

REMARKS

In the Advisory Action mailed January 15, 2003, the rejection of claims 1-5 under 35 U.S.C. §101 and §112 is maintained for the reasons set forth in the Final Rejection (Paper No. 15). The Examiner maintains that Applicants' Amendment and Response filed February 19, 2002, was not persuasive because the copies of SEQ ID No. 6 (SR-p70) of the instant application and SEQ ID No. 1 of WO 99/66946 (p73), attached to the Response to show that the polypeptides are identical, were not submitted, and that in any event, the copies of the sequences, as well as the Br. J. Cancer 2001 reference also submitted with Applicants' response, would not have been considered because Applicants had not shown good and sufficient reasons why the documents were not earlier presented.

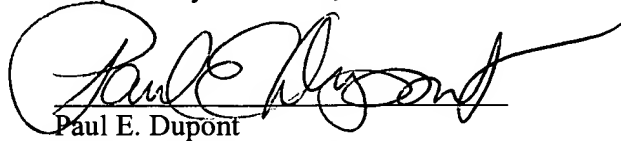
Applicants hereby request that the sequences, copies of which are resubmitted herewith, the Br. J. Cancer 2001 reference, and the Response filed February 19, 2002, be fully considered. It is submitted that the rejection under 35 U.S.C. §101 and §112 is fully met by the previous response and supporting documents, and accordingly, reconsideration and withdrawal of said rejection are respectfully requested.

Claim 3 remains rejected under 35 U.S.C. §102 for the reasons of record, namely, that subject matter of the Dequiedt et al reference falls within the scope of claim 3. The rejection is believed overcome by the foregoing amendment of claim 3 to more particularly describe the amino acid sequences of SEQ ID No. 2 and 6 between residues 110 and 310 and the amino acid sequence of SEQ ID No. 8 between residue 60 and residue 260. The Dequiedt et al reference does not disclose any sequence falling within the scope of claim 3 as amended and hence does not anticipate Applicants' claims. Accordingly, the rejection should be withdrawn.

There being no remaining issues this application is believed in condition for allowance and such action is earnestly solicited.

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Respectfully submitted,



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Version With Markings to Show Changes Made

In the Claims:

Claim 3 has been amended as follows:

3. (Twice amended) A polypeptide according to Claim 1 comprising a an amino acid sequence ~~lying between:~~

~~— residue 110 and residue 310 of~~ selected from the group consisting of SEQ ID No. 2 ~~or~~
6; from residue 110 to residue 310, SEQ ID No. 6 from residue 110 to residue 310, and
~~— residue 60 and residue 260 of~~ SEQ ID No. 8 from residue 60 to residue 260.



SEQ ID No. 6 of Serial No. 09/125,005 (SR-p70)

<400> 6
Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1 5 10 15
His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
20 25 30
Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
35 40 45
Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
50 55 60
Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65 70 75 80
Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ser Val Pro Thr His
85 90 95
Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
100 105 110
Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
115 120 125
Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
130 135 140
Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
145 150 155 160
Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg
165 170 175
Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
180 185 190
Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
195 200 205
Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
210 215 220
Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
225 230 235 240
Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
245 250 255
Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
260 265 270
Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
275 280 285
Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
290 295 300
Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
305 310 315 320
Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
325 330 335
Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
340 345 350
Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
355 360 365
Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
370 375 380
Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Gln Arg Pro Ser
385 390 395 400
His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
405 410 415
Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420 425 430
Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
435 440 445
Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
450 455 460
Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
465 470 475 480
Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe
485 490 495
Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln
500 505 510
Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu
515 520 525
Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly
530 535 540
Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu
545 550 555 560
Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
565 570 575
Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
580 585 590
Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu
595 600 605
Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
610 615 620
Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
625 630 635

SEQ ID No. 1 of WO 99/66946 (p73)

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<400> 1
Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
1      5      10
His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
20     25     30
Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
35     40     45
Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
50     55     60
Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
65     70     75     80
Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
85     90     95
Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
100    105    110
Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
115    120    125
Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
130    135    140
Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
145    150    155    160
Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg
165    170    175
Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys
180    185    190
Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser
195    200    205
Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln
210    215    220
Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr
225    230    235    240
Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe
245    250    255
Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu
260    265    270
Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg
275    280    285
Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala
290    295    300
Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala
305    310    315    320
Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala
325    330    335
Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu
340    345    350
Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu
355    360    365
Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro
370    375    380
Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser
385    390    395    400
His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys
405    410    415
Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly
420    425    430
Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val
435    440    445
Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly
450    455    460
Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
465    470    475    480
Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe
485    490    495
Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln
500    505    510
Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu
515    520    525
Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly
530    535    540
Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu
545    550    555    560
Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu
565    570    575
Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His
580    585    590
Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu
595    600    605
Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln
610    615    620
Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His
625    630    635

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